

CLAIMS:

1. A method for reducing the incorporation of non-standard amino acids into a heterologous protein expressed by microorganisms comprising:
co-expressing in the microorganism at least one heterologous protein and at least one non-standard amino acid degrading protein.
2. The method of claim 1 wherein the non-standard amino acid degrading protein is a glutamate dehydrogenase, leucine dehydrogenase, a valine dehydrogenase, a glutamate/leucine/phenylalanine/valine dehydrogenase, a phenylalanine dehydrogenase, or an opine dehydrogenase.
3. The method of claim 2 wherein the non-standard amino acid degrading protein is a wild-type or K92L variant glutamate dehydrogenase from *Escherichia coli*, a leucine dehydrogenase from *Bacillus cereus*, a leucine dehydrogenase from *Bacillus subtilis*, a leucine dehydrogenase from *Nostoc sp.* a leucine dehydrogenase from *Shewanella oneidensis*, a valine dehydrogenase from *Streptomyces avermitilis*, or a glutamate/leucine/phenylalanine/valine dehydrogenase from *Nitrosomonas europaea*.
4. The method of claim 3 wherein the non-standard amino acid degrading protein has a sequence selected from SEQ ID NO:2, 4, 6, 8, 10, 12, 14, or 16.
5. The method of claim 4 wherein the non-standard amino acid is encoded by a DNA molecule having a sequence selected from SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15.
6. The method of claim 2 wherein the non-standard amino acid degrading protein is a lysine 92 leucine variant of glutamate dehydrogenase.
7. The method of claim 6 wherein the variant glutamate dehydrogenase is from *Escherichia coli*.
8. The method of claim 1 wherein the microorganism is *Escherichia coli*.
9. The method of claim 1 wherein at least one of the expressed heterologous protein(s) is a somatotropin.
10. The method of claim 9 wherein the somatotropin is selected from the group consisting of human, equine, bovine, ovine, porcine, canine, or feline somatotropin.
11. The method of claim 9 wherein the somatotropin is bovine somatotropin.

12. The method of claim 1 wherein the microorganism is *Escherichia coli* (*E. coli*); wherein the non-standard amino acid degrading protein is *E. coli* glutamate dehydrogenase or a lysine 92 leucine variant of *E. coli* glutamate dehydrogenase; and wherein the heterologous protein is bovine somatotropin.
13. The method of claim 1 wherein the non-standard amino acid degrading protein is a leucine dehydrogenase from *Bacillus cereus*, a leucine dehydrogenase from *Bacillus subtilis*, a leucine dehydrogenase from *Nostoc sp.*, a leucine dehydrogenase from *Shewanella oneidensis*, a valine dehydrogenase from *Streptomyces avermitilis*, or a glutamate/leucine/phenylalanine/valine dehydrogenase from *Nitrosomonas europaea*; and wherein the heterologous protein is bovine somatotropin.
14. The method of claim 1 wherein the heterologous protein and the non-standard amino acid degrading protein are expressed from a single expression vector.
15. The method of claim 1 wherein the heterologous protein and the non-standard amino acid degrading protein are expressed from at least two distinct expression vectors.
16. The method of claim 1 wherein the non-standard amino acid is norleucine.
17. The method of claim 1 wherein the non-standard amino acid degrading protein is selected from the group consisting of: a glutamate dehydrogenase, a phenylalanine dehydrogenase, a valine dehydrogenase, a leucine dehydrogenase, a glutamate/leucine/phenylalanine/valine dehydrogenase and an opine dehydrogenase; and wherein the non-standard amino acid is selected from the group comprising: norleucine, norvaline, beta-methylnorleucine, and homoisoleucine.
18. The method of claim 17 wherein the non-standard amino acid is norleucine or norvaline.
19. A recombinant *Escherichia coli* glutamate dehydrogenase protein comprising a lysine 92 to leucine variation.
20. The recombinant protein of claim 19 having the sequence of SEQ ID NO:4.
21. A recombinant DNA molecule capable of encoding an *Escherichia coli* glutamate dehydrogenase variant; wherein the variant comprises a variation in the codon encoding amino acid 92, as compared to the wild-type DNA sequence, such that it encodes leucine instead of lysine.
22. The DNA molecule of claim 21 comprising the sequence of SEQ ID NO:3.

23. The DNA molecule of claim 21 capable of encoding a protein comprising the sequence of SEQ ID NO:4.
24. An *Escherichia coli* (*E. coli*) cell comprising a DNA sequence encoding an *E. coli* glutamate dehydrogenase; wherein said glutamate dehydrogenase comprises a lysine 92 to leucine variation.
25. The cell of claim 24 wherein the cell comprises a DNA molecule comprising the sequence of SEQ ID NO:3.
26. The cell of claim 24 wherein the cell expresses a protein comprising the sequence of SEQ ID NO:4.
27. A method of isolating a protein from a microorganism comprising:
 - a) co-expressing in a microorganism at least one heterologous protein and at least one non-standard amino acid degrading protein;
 - b) isolating the heterologous protein from the microorganism.
28. A method of isolating a protein comprising:
isolating at least one heterologous protein from a microorganism; wherein said microorganism co-expresses at least one heterologous protein and at least one non-standard amino acid degrading protein.
29. The method of either claim 27 or claim 28 wherein the non-standard amino acid degrading protein is selected from the group consisting of a glutamate dehydrogenase, a phenylalanine dehydrogenase, a leucine dehydrogenase, a valine dehydrogenase, a glutamate/leucine/phenylalanine/valine dehydrogenase, and an opine dehydrogenase.
30. The method of claim 29 wherein the non-standard amino acid is norleucine.
31. The method of claim 29 wherein the non-standard amino acid degrading protein is a glutamate dehydrogenase, a leucine dehydrogenase, a valine dehydrogenase, or a glutamate/leucine/phenylalanine/valine dehydrogenase.
32. The method of claim 31 wherein the non-standard amino acid degrading enzyme is a wild-type or K92L variant glutamate dehydrogenase from *Escherichia coli*, a leucine dehydrogenase from *Bacillus cereus*, a leucine dehydrogenase from *Bacillus subtilis*, a leucine dehydrogenase from *Nostoc* sp. a leucine dehydrogenase from *Shewanella*

oneidensis, a valine dehydrogenase from *Streptomyces avermitilis*, or a glutamate/leucine/phenylalanine/valine dehydrogenase from *Nitrosomonas europaea*.

33. The method of claim 32 wherein the non-standard amino acid degrading enzyme is a glutamate dehydrogenase comprising a lysine 92 to leucine variation.
34. The method of claim 31 wherein the non-standard amino acid degrading enzyme is a leucine dehydrogenase from *Bacillus cereus*, a leucine dehydrogenase from *Bacillus subtilis*, a leucine dehydrogenase from *Nostoc sp.* a leucine dehydrogenase from *Shewanella oneidensis*, a valine dehydrogenase from *Streptomyces avermitilis*, or a glutamate/leucine/phenylalanine/valine dehydrogenase from *Nitrosomonas europaea*.
35. The method of either claim 27 or claim 28 wherein the microorganism is *Escherichia coli*.
36. The method of claim 35 wherein the non-standard amino acid degrading enzyme is a glutamate dehydrogenase, a leucine dehydrogenase, a valine dehydrogenase, or a glutamate/leucine/phenylalanine/valine dehydrogenase.
37. The method of either claim 27 or claim 28 wherein the microorganism is *Escherichia coli* (*E. coli*); and
wherein the non-standard amino acid degrading enzyme is a lysine 92 to leucine variant of *E. coli* glutamate dehydrogenase, a leucine dehydrogenase, a valine dehydrogenase, or glutamate/leucine/phenylalanine/valine dehydrogenase; and
wherein at least one heterologous protein is a bovine somatotropin.
38. The method either of claims 27 or 28 wherein the non-standard amino acid degrading protein is selected from the group consisting of: a glutamate dehydrogenase, a phenylalanine dehydrogenase, a valine dehydrogenase, a leucine dehydrogenase, and a glutamate/leucine/phenylalanine/valine dehydrogenase; and wherein the non-standard amino acid is selected from the group comprising: norleucine, norvaline, beta-methylnorleucine, and homoisoleucine.
39. The method of claim 38 wherein the non-standard amino acid is norleucine or norvaline.
40. The method of either claim 27 or 28 wherein the non-standard amino acid degrading protein is capable of degrading norleucine.

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41. The method of either claim 27 or 28 wherein the percentage of heterologous protein containing norleucine is substantially zero.
42. The method of claim 1 wherein the heterologous protein and/or the norleucine degrading protein is expressed from a location in the microorganism's genome.